

AMENDMENTS TO THE CLAIMS

Please amend the claims as follows.

Please cancel claims 61, 63 and 64, without prejudice or disclaimer.

This listing will replace all prior versions and listings of claims in this application:

Listing of Claims:

Claim 43 (Currently amended): A method for forming a catalogued nucleic acid library from an initial organism sample comprised of heterogeneous organisms, said method comprising:

(i) (a) forming a derived organism sample from the initial heterogeneous organism sample by subjecting all or a part of said initial heterogeneous organism sample to a method of selection, such that proportional representations of the constituents in said derived organism sample are adjusted to advantage by performing in any order, and at least one time, at least one step selected from the group consisting of: (i) subjecting all or a part of said initial heterogeneous organism sample to a method of selection, and (ii) recovering a fraction of said initial organism sample having at least one desired characteristic;

(b) isolating an initial nucleic acid sample from said derived organism sample of step (a);

(c) forming a derived nucleic acid library from said isolated initial nucleic acid sample of step (b), such that the proportional representations of the constituents in said derived nucleic acid library are adjusted to advantage by performing in any order, and at least one time, a at least one step comprising selected from the group consisting of: (i) subjecting all or a part of said initial nucleic acid sample to a period of selection, (ii) recovering a fraction of said initial organism nucleic acid sample having at least one desired characteristic, and (iii) assembling all or a part of said derived nucleic acid sample into a nucleic acid library;

thereby forming a catalogued nucleic acid library from the initial organism sample comprised of heterogeneous organisms; or

(ii) the method of (i), wherein the method of selection in step (i)(a) is a positive or a negative selection, or comprises both a positive and a negative selection.

Claim 44 (withdrawn – currently amended): The method of forming a catalogued nucleic acid library according to claim 43 wherein the subjecting all or a part of said initial

heterogeneous organism sample to a method of selection of step (a) further comprises: (i) resolving heterogeneity of the initial heterogeneous organism sample according to at least one organism marker such that the initial derived organism sample is normalized with respect to organisms exhibiting the at least one common organism marker before the subjecting all or a part of said initial organism sample to a method of selection; or (ii) resolving heterogeneity of the organism sample after the selection step of (a) but before step (b) by normalizing the initial organism sample with respect to organisms exhibiting the at least one common organism marker.

Claim 45 (withdrawn – currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 44 wherein the at least one organism marker [[is]] comprises a 16S rRNA content or organisms in the derived organism sample.

Claim 46 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 43 wherein the subjecting all or a part of said initial heterogeneous organism sample to a method of selection of step (a) comprises selecting resolving heterogeneity of said initial heterogeneous organism sample using according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms exhibiting the selected at least one organism marker.

Claim 47 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 46 wherein the selected organisms in the derived organism sample exhibit increased 16S rRNA content or 18S rRNA content compared to those in the unselected initial organism sample.

Claim 48 (withdrawn – currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim [[43]] 44 wherein step (a) further comprises initially resolving heterogeneity of said initial heterogeneous organism sample according to at least two organism markers ~~such that the derived organism sample is normalized with respect to organisms exhibiting the at least two organism markers~~.

Claim 49 (withdrawn – currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 43 wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived

nucleic acid library is normalized with respect to the nucleic acids exhibiting the at least one organism marker.

Claim 50 (withdrawn - currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 49 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

Claim 51 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 43 wherein step (c) further comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids exhibiting the at least one nucleic acid marker.

Claim 52 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 51 wherein the at least one nucleic acid marker is G+C content of the nucleic acids in the derived nucleic acid library.

Claim 53 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 43 wherein step (c) further comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids exhibiting each of said ~~at least two organism nucleic acid~~ markers.

Claim 54 (withdrawn - currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 43 wherein ~~step (a) comprises resolving heterogeneity of the initial organism sample according to at least one organism marker such that the derived organism sample is normalized with respect to organisms exhibiting said at least one organism marker, and also wherein~~ step (c) comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids exhibiting the at least one nucleic acid marker.

Claim 55 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim [[43]] 44 wherein the at least one organism marker ~~comprises is 16S rRNA content or 18S rRNA content of organisms in the derived organism sample.~~

Claim 56 (currently amended): The method of ~~forming a catalogued nucleic acid library according to claim [[43]] 44~~ wherein the at least one ~~nucleic acid~~ organism marker comprises is G+C content of the nucleic acids in the derived nucleic acid library.

Claim 57 (withdrawn - currently amended): The method of ~~forming a catalogued nucleic acid library according to claim 43~~ wherein ~~step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is normalized with respect to organisms that exhibit the at least one organism marker, and also wherein~~ step (c) comprises resolving heterogeneity of the initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

Claim 58 (withdrawn – currently amended): The method of ~~forming a catalogued nucleic acid library according to claim [[57]] 81~~ wherein the at least one organism marker [[is]] comprises 16S rRNA content or 18S rRNA content ~~of organisms in the derived organism sample~~.

Claim 59 (withdrawn - currently amended): The method of ~~forming a catalogued nucleic acid library according to claim [[57]] 81~~ wherein the at least one nucleic acid marker [[is]] comprises G+C content of the nucleic acids in the derived nucleic acid library.

Claim 60 (withdrawn - currently amended): The method of ~~forming a catalogued nucleic acid library according to claim [[43]] 80~~ wherein ~~step (a) comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is normalized with respect to organisms exhibiting the at least one organism marker, and also wherein~~ step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids exhibiting each of said at least two nucleic acid markers.

Claim 61 (canceled)

Claim 62 (withdrawn - currently amended): The method of ~~forming a catalogued nucleic acid library according to claim [[43]] 80~~ wherein ~~step (a) comprises resolving heterogeneity of~~

said initial organism sample according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms exhibiting the at least one organism marker, and also wherein step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids that exhibit the at least one nucleic acid marker.

Claim 63 and claim 64 (canceled)

Claim 65 (currently amended): The method of ~~forming a catalogued nucleic acid library according to claim [[43]] 80~~ wherein step (a) ~~comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms exhibiting the at least one organism marker, and also wherein~~ step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.

Claim 66 (currently amended): The method of ~~forming a catalogued nucleic acid library according to claim 65~~ wherein the at least one organism marker [[is]] comprises 16S rRNA content or 18S rRNA content ~~of organisms in the derived organism sample~~.

Claim 67 (currently amended): The method of ~~forming a catalogued nucleic acid library according to claim 65~~ wherein the at least one nucleic acid marker [[is]] comprises G+C content of nucleic acids ~~in the derived nucleic acid library~~.

Claim 68 (currently amended): The method of ~~forming a catalogued nucleic acid library according to claim [[43]] 82~~ wherein step (a) ~~comprises resolving heterogeneity of said initial organism sample according to at least one organism marker such that the derived organism sample is selectively enriched with respect to organisms that exhibit the at least one organism marker, and also wherein~~ step (c) comprises resolving heterogeneity of said initial nucleic acid sample according to at least two nucleic acid markers such that the derived nucleic acid library is advantageously adjusted with respect to nucleic acids that exhibit each of said at least two nucleic acid markers.

Claim 69 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 68 wherein the at least one organism marker [[is]] comprises 16S rRNA content or 18S rRNA content of nucleic acids in the derived nucleic acid library.

Claim 70 (withdrawn - currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim [[43]] 82 wherein step (a) comprises resolving heterogeneity of ~~said initial organism sample according to at least two organism markers such that the derived organism sample is advantageously adjusted with respect to organisms that exhibit each of said at least two organism markers, and also wherein~~ step (c) comprises resolving heterogeneity of ~~said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is normalized with respect to nucleic acids that exhibit that at least one nucleic acid marker.~~

Claim 71 (withdrawn – currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 70 wherein the at least one nucleic acid marker [[is]] comprises the G+C content of nucleic acids ~~in the derived nucleic acid library.~~

Claim 72 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim [[43]] 82 wherein step (a) comprises resolving heterogeneity of ~~said initial organism sample according to at least two organism markers such that the derived organism sample is advantageously adjusted with respect to organisms exhibiting each of said at least two organism markers, and also wherein~~ step (c) comprises resolving heterogeneity of ~~said initial nucleic acid sample according to at least one nucleic acid marker such that the derived nucleic acid library is selectively enriched with respect to nucleic acids that exhibit the at least one nucleic acid marker.~~

Claim 73 (currently amended): The method of ~~forming a catalogued nucleic acid library according to~~ claim 72 wherein the at least one nucleic acid marker [[is]] comprises G+C content of the nucleic acids in the derived nucleic acid library.

Claim 74 (currently amended): The method of claim 80 ~~forming a catalogued nucleic acid library according to any of claims 43-73~~ wherein step (b) further comprises isolating genomic DNA from the derived organism sample, and where step (c) further comprises forming a genomic DNA library, thereby forming a catalogued genomic DNA library.

Claim 75 (currently amended): The method of claim 43 forming a nucleic acid DNA library according to any of claims 43-73 wherein step (b) comprises isolating genomic gene cluster DNA from the derived organism sample, and wherein step (c) further comprises forming a genomic gene cluster DNA library, thereby forming a catalogued genomic gene cluster DNA library.

Claim 76 (withdrawn – currently amended): The method of claim 43, forming a catalogued nucleic acid library according to any of claims 43-73 wherein step (b) comprises isolating RNA from the derived organism sample, and wherein step (c) comprises forming a cDNA library, thereby forming a catalogued cDNA library.

Claim 77 (currently amended): The method of forming a catalogued nucleic acid library according to claim 43 wherein step (a) further comprises forming a derived organism sample that consists essentially of essentially only direct environmental organisms, thereby forming a catalogued nucleic acid library from essentially only direct environmental organisms.

Claim 78 (currently amended): The method of forming a catalogued nucleic acid library according to claim [[43]] 80 wherein step (a) comprises forming a derived organism sample that consists essentially of essentially only direct environmental organisms, and wherein step (b) comprises isolating genomic DNA from the derived organism sample, and also wherein step (c) further comprises forming a genomic DNA library, thereby forming a catalogued genomic DNA library from essentially only direct environmental organisms.

Claim 79 (currently amended): The method of forming a catalogued nucleic acid library according to claim [[43]] 82 wherein step (a) further comprises forming a derived organism sample that consists essentially of essentially only direct environmental organisms, and wherein step (b) comprises isolating genomic gene cluster DNA from the derived organism sample, and also wherein step (c) further comprises forming a genomic gene cluster DNA library, thereby forming a catalogued genomic gene cluster DNA library from essentially only direct environmental organisms.

Claim 80 (new): A method for forming a catalogued nucleic acid library from an initial organism sample comprised of heterogeneous organisms, said method comprising:

(a) forming a derived organism sample from the initial heterogeneous organism sample, such that proportional representations of the constituents in said derived organism sample are adjusted to advantage by recovering a fraction of said initial heterogeneous organism sample having at least one desired characteristic;

(b) isolating an initial nucleic acid sample from said derived organism sample; and

(c) forming a derived nucleic acid library from said isolated initial nucleic acid sample of step (b), such that the proportional representations of the constituents in said derived nucleic acid library are adjusted to advantage by performing in any order, and at least one time, a ~~at least one~~ step comprising (i) subjecting all or a part of said initial nucleic acid sample to a period of selection, (ii) recovering a fraction of said initial nucleic acid sample having at least one desired characteristic, and (iii) assembling all or a part of said derived nucleic acid sample into a nucleic acid library;

thereby forming a catalogued nucleic acid library from the initial heterogeneous organism sample comprised of heterogeneous organisms.

Claim 81 (new): The method of claim 80 wherein the recovering a fraction of said initial heterogeneous organism sample having at least one desired characteristic of step (a) comprises recovering the fraction of said initial heterogeneous organism sample by selecting and recovering organisms exhibiting at least one common organism marker.

Claim 82 (new): A method for forming a catalogued nucleic acid library from an initial organism sample comprised of heterogeneous organisms, said method comprising:

(a) forming a derived organism sample from the initial heterogeneous organism sample, such that proportional representations of the constituents in said derived organism sample are adjusted to advantage by performing in any order both (i) subjecting all or a part of said initial heterogeneous organism sample to a method of selection, and (ii) recovering a fraction of said initial heterogeneous organism sample having at least one desired characteristic;

(b) isolating an initial nucleic acid sample from said derived organism sample; and

(c) forming a derived nucleic acid library from said isolated initial nucleic acid sample of step (b), such that the proportional representations of the constituents in said derived nucleic acid library are adjusted to advantage by performing in any order, and at least one time, a ~~at least one~~ step comprising (i) subjecting all or a part of said initial nucleic acid sample to a

period of selection, (ii) recovering a fraction of said initial nucleic acid sample having at least one desired characteristic, and (iii) assembling all or a part of said derived nucleic acid sample into a nucleic acid library;

thereby forming a catalogued nucleic acid library from the initial heterogeneous organism sample comprised of heterogeneous organisms.